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SEQUENCE LISTING

<110> The Scripps Research Institute
The Regents of the University of California
Wu, Eugene
Nemerow, Glen R.
Stewart, Phoebe

<120> MODIFIED FIBER PROTEINS FOR EFFICIENT
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Tyr	Asp	Thr	Glu	Thr	Gly	Pro	Pro	Thr	Val	Pro	Phe	Leu	Thr	Pro	Pro	
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ggt ggc atg cgt ata aat aac aac ttg tta att cta gat gtg gat tac Gly Gly Met Arg Ile Asn Asn Asn Leu Leu Ile Leu Asp Val Asp Tyr	260	265	270	816
cca ttt gat gct caa aca aaa cta cgt ctt aaa ctg ggg cag gga ccc Pro Phe Asp Ala Gln Thr Lys Leu Arg Leu Lys Leu Gly Gln Gly Pro	275	280	285	864
ctg tat att aat gca tct cat aac ttg gac ata aac tat aac aga ggc Leu Tyr Ile Asn Ala Ser His Asn Leu Asp Ile Asn Tyr Asn Arg Gly	290	295	300	912
cta tac ctt ttt aat gca tca aac aat act aaa aaa ctg gaa gtt agc Leu Tyr Leu Phe Asn Ala Ser Asn Asn Thr Lys Lys Leu Glu Val Ser	305	310	315	960
ata aaa aaa tcc agt gga cta aac ttt gat aat act gcc ata gct ata Ile Lys Lys Ser Ser Gly Leu Asn Phe Asp Asn Thr Ala Ile Ala Ile	325	330	335	1008
aat gca gga aag ggt ctg gag ttt gat aca aac aca tct gag tct cca Asn Ala Gly Lys Gly Leu Glu Phe Asp Thr Asn Thr Ser Glu Ser Pro	340	345	350	1056
gat atc aac cca ata aaa act aaa att ggc tct ggc att gat tac aat Asp Ile Asn Pro Ile Lys Thr Lys Ile Gly Ser Gly Ile Asp Tyr Asn	355	360	365	1104
gaa aac ggt gcc atg att act aaa ctt gga gcg ggt tta agc ttt gac Glu Asn Gly Ala Met Ile Thr Lys Leu Gly Ala Gly Leu Ser Phe Asp	370	375	380	1152
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ctg tgg aca acc cca gac cca tct cct aac tgc aga att cat tca gat Leu Trp Thr Thr Pro Asp Pro Ser Pro Asn Cys Arg Ile His Ser Asp	405	410	415	1248
aat gac tgc aaa ttt act ttg gtt ctt aca aaa tgt ggg agt caa gta Asn Asp Cys Lys Phe Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Val	420	425	430	1296
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Lys Asn Asn Ile Val Ser Gln Val Tyr Leu His Gly Asp Lys Thr Lys	
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 35 40 45
 Leu Arg Val Ser Glu Pro Leu Asp Thr Ser His Gly Met Leu Ala Leu
 50 55 60
 Lys Met Gly Ser Gly Leu Thr Leu Asp Lys Ala Gly Asn Leu Thr Ser
 65 70 75 80
 Gln Asn Val Thr Thr Val Thr Gln Pro Leu Lys Lys Thr Lys Ser Asn
 85 90 95
 Ile Ser Leu Asp Thr Ser Ala Pro Leu Thr Ile Thr Ser Gly Ala Leu
 100 105 110
 Thr Val Ala Thr Thr Ala Pro Leu Ile Val Thr Ser Gly Ala Leu Ser
 115 120 125
 Val Gln Ser Gln Ala Pro Leu Thr Val Gln Asp Ser Lys Leu Ser Ile
 130 135 140
 Ala Thr Lys Gly Pro Ile Thr Val Ser Asp Gly Lys Leu Ala Leu Gln
 145 150 155 160
 Thr Ser Ala Pro Leu Ser Gly Ser Asp Ser Asp Thr Leu Thr Val Thr
 165 170 175
 Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asn Met
 180 185 190
 Glu Asp Pro Ile Tyr Val Asn Asn Gly Lys Ile Gly Ile Lys Ile Ser

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		195					200					205			
Gly	Pro	Leu	Gln	Val	Ala	Gln	Asn	Ser	Asp	Thr	Leu	Thr	Val	Val	Thr
	210					215					220				
Gly	Pro	Gly	Val	Thr	Val	Glu	Gln	Asn	Ser	Leu	Arg	Thr	Lys	Val	Ala
225					230					235					240
Gly	Ala	Ile	Gly	Tyr	Asp	Ser	Ser	Asn	Asn	Met	Glu	Ile	Lys	Thr	Gly
				245						250					
Gly	Gly	Met	Arg	Ile	Asn	Asn	Asn	Leu	Leu	Ile	Leu	Asp	Val	Asp	Tyr
			260					265					270		
Pro	Phe	Asp	Ala	Gln	Thr	Lys	Leu	Arg	Leu	Lys	Leu	Gly	Gln	Gly	Pro
		275					280					285			
Leu	Tyr	Ile	Asn	Ala	Ser	His	Asn	Leu	Asp	Ile	Asn	Tyr	Asn	Arg	Gly
						295					300				
Leu	Tyr	Leu	Phe	Asn	Ala	Ser	Asn	Asn	Thr	Lys	Lys	Leu	Glu	Val	Ser
305					310					315					320
Ile	Lys	Lys	Ser	Ser	Gly	Leu	Asn	Phe	Asp	Asn	Thr	Ala	Ile	Ala	Ile
				325					330					335	
Asn	Ala	Gly	Lys	Gly	Leu	Glu	Phe	Asp	Thr	Asn	Thr	Ser	Glu	Ser	Pro
			340					345					350		
Asp	Ile	Asn	Pro	Ile	Lys	Thr	Lys	Ile	Gly	Ser	Gly	Ile	Asp	Tyr	Asn
		355					360					365			
Glu	Asn	Gly	Ala	Met	Ile	Thr	Lys	Leu	Gly	Ala	Gly	Leu	Ser	Phe	Asp
						375					380				
Asn	Ser	Gly	Ala	Ile	Thr	Ile	Gly	Asn	Lys	Asn	Asp	Asp	Lys	Leu	Thr
385					390					395					400
Leu	Trp	Thr	Thr	Pro	Asp	Pro	Ser	Pro	Asn	Cys	Arg	Ile	His	Ser	Asp
				405					410					415	
Asn	Asp	Cys	Lys	Phe	Thr	Leu	Val	Leu	Thr	Lys	Cys	Gly	Ser	Gln	Val
			420					425					430		
Leu	Ala	Thr	Val	Ala	Ala	Leu	Ala	Val	Ser	Gly	Asp	Leu	Ser	Ser	Met
			435				440					445			
Thr	Gly	Thr	Val	Ala	Ser	Val	Ser	Ile	Phe	Leu	Arg	Phe	Asp	Gln	Asn
						455					460				
Gly	Val	Leu	Met	Glu	Asn	Ser	Ser	Leu	Lys	Lys	His	Tyr	Trp	Asn	Phe
465					470					475					480
Arg	Asn	Gly	Asn	Ser	Thr	Asn	Ala	Asn	Pro	Tyr	Thr	Asn	Ala	Val	Gly
				485					490					495	
Phe	Met	Pro	Asn	Leu	Leu	Ala	Tyr	Pro	Lys	Thr	Gln	Ser	Gln	Thr	Ala
			500					505					510		
Lys	Asn	Asn	Ile	Val	Ser	Gln	Val	Tyr	Leu	His	Gly	Asp	Lys	Thr	Lys
			515				520					525			
Pro	Met	Ile	Leu	Thr	Ile	Thr	Leu	Asn	Gly	Thr	Ser	Glu	Ser	Thr	Glu
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Thr	Ser	Glu	Val	Ser	Thr	Tyr	Ser	Met	Ser	Phe	Thr	Trp			

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<210> 34
<211> 1746
<212> DNA
<213> Adenovirus serotype 5 fiber
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<220>
<221> CDS
<222> (1) ... (1746)
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<400> 34

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atg Met 1	aag Lys	cgc Arg	gca Ala	aga Arg 5	ccg Pro	tct Ser	gaa Glu	gat Asp	acc Thr 10	ttc Phe	aac Asn	ccc Pro	gtg Val	tat Tyr 15	cca Pro	48
tat Tyr	gac Asp	acg Thr	gaa Glu 20	acc Thr	ggg Gly	cct Pro	cca Pro	act Thr 25	gtg Val	cct Pro	ttt Phe	ctt Leu	act Thr 30	cct Pro	ccc Pro	96
ttt Phe	gta Val	tcc Ser 35	ccc Pro	aat Asn	ggg Gly	ttt Phe	caa Gln 40	gag Glu	agt Ser	ccc Pro	cct Pro	ggg Gly 45	gta Val	ctc Leu	tct Ser	144
ttg Leu	cgc Arg 50	cta Leu	tcc Ser	gaa Glu	cct Pro	cta Leu 55	gtt Val	acc Thr	tcc Ser	aat Asn	ggc Gly 60	atg Met	ctt Leu	gcg Ala	ctc Leu	192
aaa Lys 65	atg Met	ggc Gly	aac Asn	ggc Gly	ctc Leu 70	tct Ser	ctg Leu	gac Asp	gag Glu	gcc Ala 75	ggc Gly	aac Asn	ctt Leu	acc Thr	tcc Ser 80	240
caa Gln	aat Asn	gta Val	acc Thr	act Thr 85	gtg Val	agc Ser	cca Pro	cct Pro	ctc Leu 90	aaa Lys	aaa Lys	acc Thr	aag Lys	tca Ser 95	aac Asn	288
ata Ile	aac Asn	ctg Leu	gaa Glu 100	ata Ile	tct Ser	gca Ala	ccc Pro	ctc Leu 105	aca Thr	gtt Val	acc Thr	tca Ser	gaa Glu 110	gcc Ala	cta Leu	336
act Thr	gtg Val	gct Ala 115	gcc Ala	gcc Ala	gca Ala	cct Pro	cta Leu 120	atg Met	gtc Val	gcg Ala	ggc Gly	aac Asn 125	aca Thr	ctc Leu	acc Thr	384
atg Met	caa Gln 130	tca Ser	cag Gln	gcc Ala	ccg Pro	cta Leu 135	acc Thr	gtg Val	cac His	gac Asp	tcc Ser 140	aaa Lys	ctt Leu	agc Ser	att Ile	432
gcc Ala 145	acc Thr	caa Gln	gga Gly	ccc Pro	ctc Leu 150	aca Thr	gtg Val	tca Ser	gaa Glu	gga Gly 155	aag Lys	cta Leu	gcc Ala	ctg Leu	caa Gln 160	480
aca Thr	tca Ser	ggc Gly	ccc Pro	ctc Leu 165	acc Thr	acc Thr	acc Thr	gat Asp	agc Ser 170	agt Ser	acc Thr	ctt Leu	act Thr	atc Ile 175	act Thr	528
gcc Ala	tca Ser	ccc Pro	cct Pro 180	cta Leu	act Thr	act Thr	gcc Ala	act Thr 185	ggg Gly	agc Ser	ttg Leu	ggc Gly	att Ile 190	gac Asp	ttg Leu	576
aaa Lys	gag Glu	ccc Pro 195	att Ile	tat Tyr	aca Thr	caa Gln	aat Asn 200	gga Gly	aaa Lys	cta Leu	gga Gly 205	cta Leu	aag Lys	tac Tyr	ggg Gly	624
gct Ala	cct Pro 210	ttg Leu	cat His	gta Val	aca Thr	gac Asp 215	gac Asp	cta Leu	aac Asn	act Thr	ttg Leu 220	acc Thr	gta Val	gca Ala	act Thr	672
ggg Gly 225	cca Pro	ggg Gly	gtg Val	act Thr	att Ile 230	aat Asn	aat Asn	act Thr	tcc Ser	ttg Leu 235	caa Gln	act Thr	aaa Lys	gtt Val	act Thr 240	720
gga Gly	gcc Pro	ttg Gly	ggg Gly	ttt Gly	gat Thr	tca Ala	caa Gln	ggc Gly	aat Thr	atg Thr	caa Gln	ctt Thr	aat Thr	gta Val	gca Ala	768

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Gly	Ala	Leu	Gly	Phe 245	Asp	Ser	Gln	Gly	Asn 250	Met	Gln	Leu	Asn	Val 255	Ala		
gga	gga	cta	agg	att	gat	tct	caa	aac	aga	cgc	ctt	ata	ctt	gat	gtt	816	
Gly	Gly	Leu	Arg 260	Ile	Asp	Ser	Gln	Asn 265	Arg	Arg	Leu	Ile	Leu 270	Asp	Val		
agt	tat	ccg	ttt	gat	gct	caa	aac	caa	cta	aat	cta	aga	cta	gga	cag	864	
Ser	Tyr	Pro 275	Phe	Asp	Ala	Gln	Asn 280	Gln	Leu	Asn	Leu	Arg	Leu 285	Gly	Gln		
ggc	cct	ctt	ttt	ata	aac	tca	gcc	cac	aac	ttg	gat	att	aac	tac	aac	912	
Gly	Pro 290	Leu	Phe	Ile	Asn	Ser 295	Ala	His	Asn	Leu	Asp 300	Ile	Asn	Tyr	Asn		
aaa	ggc	ctt	tac	ttg	ttt	aca	gct	tca	aac	aat	tcc	aaa	aag	ctt	gag	960	
Lys 305	Gly	Leu	Tyr	Leu 310	Phe	Thr	Ala	Ser	Asn	Asn 315	Ser	Lys	Lys	Leu	Glu 320		
gtt	aac	cta	agc	act	gcc	aag	ggg	ttg	atg	ttt	gac	gct	aca	gcc	ata	1008	
Val	Asn	Leu	Ser	Thr 325	Ala	Lys	Gly	Leu	Met 330	Phe	Asp	Ala	Thr 335				
gcc	att	aat	gca	gga	gat	ggg	ctt	gaa	ttt	ggg	tca	cct	aat	gca	cca	1056	
Ala	Ile	Asn	Ala 340	Gly	Asp	Gly	Leu	Glu 345	Phe	Gly	Ser	Pro	Asn 350	Ala	Pro		
aac	aca	aat	ccc	ctc	aaa	aca	aaa	att	ggc	cat	ggc	cta	gaa	ttt	gat	1104	
Asn	Thr	Asn 355	Pro	Leu	Lys	Thr	Lys 360	Ile	Gly	His	Gly	Leu 365	Glu	Phe	Asp		
tca	aac	aag	gct	atg	gtt	cct	aaa	cta	gga	act	ggc	ctt	agt	ttt	gac	1152	
Ser	Asn 370	Lys	Ala	Met	Val	Pro 375	Lys	Leu	Gly	Thr	Gly 380	Leu	Ser	Phe	Asp		
agc	aca	ggg	gcc	att	aca	gta	gga	aac	aaa	aat	aat	gat	aag	cta	act	1200	
Ser	Thr	Gly	Ala	Ile 390	Thr	Val	Gly	Asn	Lys	Asn 395	Asn	Asp	Lys	Leu	Thr 400		
ttg	tgg	acc	aca	cca	gct	cca	tct	cct	aac	tgt	aga	cta	aat	gca	gag	1248	
Leu	Trp	Thr	Thr	Pro 405	Ala	Pro	Ser	Pro	Asn 410	Cys	Arg	Leu	Asn	Ala 415	Glu		
aaa	gat	gct	aaa	ctc	act	ttg	gtc	tta	aca	aaa	tgt	ggc	agt	caa	ata	1296	
Lys	Asp	Ala 420	Lys	Leu	Thr	Leu	Val	Leu 425	Thr	Lys	Cys	Gly	Ser 430	Gln	Ile		
ctt	gct	aca	gtt	tca	gtt	ttg	gct	gtt	aaa	ggc	agt	ttg	gct	cca	ata	1344	
Leu	Ala	Thr 435	Val	Ser	Val	Leu	Ala 440	Val	Lys	Gly	Ser	Leu 445	Ala	Pro	Ile		
tct	gga	aca	gtt	caa	agt	gct	cat	ctt	att	ata	aga	ttt	gac	gaa	aat	1392	
Ser	Gly 450	Thr	Val	Gln	Ser	Ala 455	His	Leu	Ile	Ile	Arg 460	Phe	Asp	Glu	Asn		
gga	gtg	cta	cta	aac	aat	tcc	ttc	ctg	gac	cca	gaa	tat	tgg	aac	ttt	1440	
Gly 465	Val	Leu	Leu	Asn 470	Asn	Ser	Phe	Leu	Asp	Pro 475	Glu	Tyr	Trp	Asn 480	Phe		
aga	aat	gga	gat	ctt	act	gaa	ggc	aca	gcc	tat	aca	aac	gct	gtt	gga	1488	
Arg	Asn	Gly	Asp	Leu	Thr	Glu	Gly	Thr	Ala	Tyr	Thr	Asn	Ala	Val	Gly		

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485										490					495					
ttt atg cct aac cta tca gct tat cca aaa tct cac ggt aaa act gcc	Phe Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala	1536																		
	500 505 510																			
aaa agt aac att gtc agt caa gtt tac tta aac gga gac aaa act aaa	Lys Ser Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys	1584																		
	515 520 525																			
cct gta aca cta acc att aca cta aac ggt aca cag gaa aca gga gac	Pro Val Thr Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp	1632																		
	530 535 540																			
aca act cca agt gca tac tct atg tca ttt tca tgg gac tgg tct ggc	Thr Thr Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly	1680																		
	545 550 555 560																			
cac aac tac att aat gaa ata ttt gcc aca tcc tct tac act ttt tca	His Asn Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser	1728																		
	565 570 575																			
tac att gcc caa gaa taa	Tyr Ile Ala Gln Glu *	1746																		
	580																			

<210> 35
 <211> 581
 <212> PRT
 <213> Adenovirus serotype 5 fiber

<400> 35
 Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro
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 Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro
 20 25 30
 Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser
 35 40 45
 Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu
 50 55 60
 Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser
 65 70 75 80
 Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Ser Asn
 85 90 95
 Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu
 100 105 110
 Thr Val Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr
 115 120 125
 Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile
 130 135 140
 Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln
 145 150 155 160
 Thr Ser Gly Pro Leu Thr Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr
 165 170 175
 Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu
 180 185 190
 Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly
 195 200 205
 Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr
 210 215 220

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Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr
 225 230 235 240
 Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala
 245 250 255
 Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val
 260 265 270
 Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln
 275 280 285
 Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn
 290 295 300
 Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu
 305 310 315 320
 Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile
 325 330 335
 Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro
 340 345 350
 Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp
 355 360 365
 Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp
 370 375 380
 Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr
 385 390 395 400
 Leu Trp Thr Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn Ala Glu
 405 410 415
 Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile
 420 425 430
 Leu Ala Thr Val Ser Val Leu Ala Val Lys Gly Ser Leu Ala Pro Ile
 435 440 445
 Ser Gly Thr Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn
 450 455 460
 Gly Val Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe
 465 470 475 480
 Arg Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly
 485 490 495
 Phe Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala
 500 505 510
 Lys Ser Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys
 515 520 525
 Pro Val Thr Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp
 530 535 540
 Thr Thr Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly
 545 550 555 560
 His Asn Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser
 565 570 575
 Tyr Ile Ala Gln Glu
 580

<210> 36
 <211> 1098
 <212> DNA
 <213> Adenovirus serotype 37 fiber

<220>
 <221> CDS
 <222> (1) ... (1098)

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 Met Ser Lys Arg Leu Arg Val Glu Asp Asp Phe Asn Pro Val Tyr Pro
 1 5 10 15

-23-

tat	ggc	tac	gcg	cgg	aat	cag	aat	atc	ccc	ttc	ctc	act	ccc	ccc	ttt	96
Tyr	Gly	Tyr	Ala	Arg	Asn	Gln	Asn	Ile	Pro	Phe	Leu	Thr	Pro	Pro	Phe	
			20					25					30			
gtc	tcc	tcc	gat	gga	ttc	aaa	aac	ttc	ccc	cct	ggg	gta	ctg	tca	ctc	144
Val	Ser	Ser	Asp	Gly	Phe	Lys	Asn	Phe	Pro	Pro	Gly	Val	Leu	Ser	Leu	
		35					40					45				
aaa	ctg	gct	gat	cca	atc	acc	att	acc	aat	ggg	gat	gta	tcc	ctc	aag	192
Lys	Leu	Ala	Asp	Pro	Ile	Thr	Ile	Thr	Asn	Gly	Asp	Val	Ser	Leu	Lys	
	50					55					60					
gtg	gga	ggt	ggt	ctc	act	ttg	caa	gat	gga	agc	cta	act	gta	aac	cct	240
Val	Gly	Gly	Gly	Leu	Thr	Leu	Gln	Asp	Gly	Ser	Leu	Thr	Val	Asn	Pro	
	65				70					75					80	
aag	gct	cca	ctg	caa	ggt	aat	act	gat	aaa	aaa	ctt	gag	ctt	gca	tat	288
Lys	Ala	Pro	Leu	Gln	Val	Asn	Thr	Asp	Lys	Lys	Leu	Glu	Leu	Ala	Tyr	
				85					90					95		
gat	aat	cca	ttt	gaa	agt	agt	gct	aat	aaa	ctt	agt	tta	aaa	gta	gga	336
Asp	Asn	Pro	Phe	Glu	Ser	Ser	Ala	Asn	Lys	Leu	Ser	Leu	Lys	Val	Gly	
			100					105					110			
cat	gga	tta	aaa	gta	tta	gat	gaa	aaa	agt	gct	gcg	ggg	tta	aaa	gat	384
His	Gly	Leu	Lys	Val	Leu	Asp	Glu	Lys	Ser	Ala	Ala	Gly	Leu	Lys	Asp	
		115					120					125				
tta	att	ggc	aaa	ctt	gtg	ggt	tta	aca	gga	aaa	gga	ata	ggc	act	gaa	432
Leu	Ile	Gly	Lys	Leu	Val	Val	Leu	Thr	Gly	Lys	Gly	Ile	Gly	Thr	Glu	
	130					135					140					
aat	tta	gaa	aat	aca	gat	ggt	agc	agc	aga	gga	att	ggt	ata	aat	gta	480
Asn	Leu	Glu	Asn	Thr	Asp	Gly	Ser	Ser	Arg	Gly	Ile	Gly	Ile	Asn	Val	
	145				150					155					160	
aga	gca	aga	gaa	ggg	ttg	aca	ttt	gac	aat	gat	gga	tac	ttg	gta	gca	528
Arg	Ala	Arg	Glu	Gly	Leu	Thr	Phe	Asp	Asn	Asp	Gly	Tyr	Leu	Val	Ala	
			165						170					175		
tgg	aac	cca	aag	tat	gac	acg	cgc	aca	ctt	tgg	aca	aca	cca	gac	aca	576
Trp	Asn	Pro	Lys	Tyr	Asp	Thr	Arg	Thr	Leu	Trp	Thr	Thr	Pro	Asp	Thr	
			180				185						190			
tct	cca	aac	tgc	aca	att	gct	caa	gat	aag	gac	tct	aaa	ctc	act	ttg	624
Ser	Pro	Asn	Cys	Thr	Ile	Ala	Gln	Asp	Lys	Asp	Ser	Lys	Leu	Thr	Leu	
		195					200					205				
gta	ctt	aca	aag	tgt	gga	agt	caa	ata	tta	gct	aat	gtg	tct	ttg	att	672
Val	Leu	Thr	Lys	Cys	Gly	Ser	Gln	Ile	Leu	Ala	Asn	Val	Ser	Leu	Ile	
	210					215					220					
gtg	gtc	gca	gga	aag	tac	cac	atc	ata	aat	aat	aag	aca	aat	cca	aaa	720
Val	Val	Ala	Gly	Lys	Tyr	His	Ile	Ile	Asn	Asn	Lys	Thr	Asn	Pro	Lys	
	225				230					235					240	
ata	aaa	agt	ttt	act	att	aaa	ctg	cta	ttt	aat	aag	aac	gga	gtg	ctt	768
Ile	Lys	Ser	Phe	Thr	Ile	Lys	Leu	Leu	Phe	Asn	Lys	Asn	Gly	Val	Leu	
				245					250					255		

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tta gac aac tca aat ctt gga aaa gct tat tgg aac ttt aga agt gga	816
Leu Asp Asn Ser Asn Leu Gly Lys Ala Tyr Trp Asn Phe Arg Ser Gly	
	260
	265
	270
aat tcc aat gtt tcg aca gct tat gaa aaa gca att ggt ttt atg cct	864
Asn Ser Asn Val Ser Thr Ala Tyr Glu Lys Ala Ile Gly Phe Met Pro	
	275
	280
	285
aat ttg gta gcg tat cca aaa ccc agt aat tct aaa aaa tat gca aga	912
Asn Leu Val Ala Tyr Pro Lys Pro Ser Asn Ser Lys Lys Tyr Ala Arg	
	290
	295
	300
gac ata gtt tat gga act ata tat ctt ggt gga aaa cct gat cag cca	960
Asp Ile Val Tyr Gly Thr Ile Tyr Leu Gly Gly Lys Pro Asp Gln Pro	
	305
	310
	315
	320
gca gtc att aaa act acc ttt aac caa gaa act gga tgt gaa tac tct	1008
Ala Val Ile Lys Thr Thr Phe Asn Gln Glu Thr Gly Cys Glu Tyr Ser	
	325
	330
	335
atc aca ttt aac ttt agt tgg tcc aaa acc tat gaa aat gtt gaa ttt	1056
Ile Thr Phe Asn Phe Ser Trp Ser Lys Thr Tyr Glu Asn Val Glu Phe	
	340
	345
	350
gaa acc acc tct ttt acc ttc tcc tat att gcc caa gaa tga	1098
Glu Thr Thr Ser Phe Thr Phe Ser Tyr Ile Ala Gln Glu *	
	355
	360
	365

<210> 37

<211> 365

<212> PRT

<213> Adenovirus serotype 37 fiber

<400> 37

Met Ser Lys Arg Leu Arg Val Glu Asp Asp Phe Asn Pro Val Tyr Pro	
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Val Ser Ser Asp Gly Phe Lys Asn Phe Pro Pro Gly Val Leu Ser Leu	
	35 40 45
Lys Leu Ala Asp Pro Ile Thr Ile Thr Asn Gly Asp Val Ser Leu Lys	
	50 55 60
Val Gly Gly Gly Leu Thr Leu Gln Asp Gly Ser Leu Thr Val Asn Pro	
	65 70 75
Lys Ala Pro Leu Gln Val Asn Thr Asp Lys Lys Leu Glu Leu Ala Tyr	
	80 85 90
Asp Asn Pro Phe Glu Ser Ser Ala Asn Lys Leu Ser Leu Lys Val Gly	
	95 100 105
His Gly Leu Lys Val Leu Asp Glu Lys Ser Ala Ala Gly Leu Lys Asp	
	110 115 120
Leu Ile Gly Lys Leu Val Val Leu Thr Gly Lys Gly Ile Gly Thr Glu	
	125 130 135
Asn Leu Glu Asn Thr Asp Gly Ser Ser Arg Gly Ile Gly Ile Asn Val	
	140 145 150
Arg Ala Arg Glu Gly Leu Thr Phe Asp Asn Asp Gly Tyr Leu Val Ala	
	155 160 165
Trp Asn Pro Lys Tyr Asp Thr Arg Thr Leu Trp Thr Thr Pro Asp Thr	
	170 175 180
Ser Pro Asn Cys Thr Ile Ala Gln Asp Lys Asp Ser Lys Leu Thr Leu	
	185 190

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Val	Leu	Thr	Lys	Cys	Gly	Ser	Gln	Ile	Leu	Ala	Asn	Val	Ser	Leu	Ile
210						215					220				
Val	Val	Ala	Gly	Lys	Tyr	His	Ile	Ile	Asn	Asn	Lys	Thr	Asn	Pro	Lys
225					230					235					240
Ile	Lys	Ser	Phe	Thr	Ile	Lys	Leu	Leu	Phe	Asn	Lys	Asn	Gly	Val	Leu
				245					250					255	
Leu	Asp	Asn	Ser	Asn	Leu	Gly	Lys	Ala	Tyr	Trp	Asn	Phe	Arg	Ser	Gly
			260					265					270		
Asn	Ser	Asn	Val	Ser	Thr	Ala	Tyr	Glu	Lys	Ala	Ile	Gly	Phe	Met	Pro
			275				280					285			
Asn	Leu	Val	Ala	Tyr	Pro	Lys	Pro	Ser	Asn	Ser	Lys	Lys	Tyr	Ala	Arg
			290			295					300				
Asp	Ile	Val	Tyr	Gly	Thr	Ile	Tyr	Leu	Gly	Gly	Lys	Pro	Asp	Gln	Pro
305					310					315					320
Ala	Val	Ile	Lys	Thr	Thr	Phe	Asn	Gln	Glu	Thr	Gly	Cys	Glu	Tyr	Ser
				325					330					335	
Ile	Thr	Phe	Asn	Phe	Ser	Trp	Ser	Lys	Thr	Tyr	Glu	Asn	Val	Glu	Phe
			340					345					350		
Glu	Thr	Thr	Ser	Phe	Thr	Phe	Ser	Tyr	Ile	Ala	Gln	Glu			
		355					360					365			

<210> 38
 <211> 1098
 <212> DNA
 <213> Adenovirus serotype 19p fiber

<220>
 <221> CDS
 <222> (1)...(1098)

<400> 38																
atg	tca	aag	agg	ctc	cgg	gtg	gaa	gat	gac	ttc	aac	ccc	gtc	tac	ccc	48
Met	Ser	Lys	Arg	Leu	Arg	Val	Glu	Asp	Asp	Phe	Asn	Pro	Val	Tyr	Pro	
1				5					10				15			
tat	ggc	tac	gcg	cgg	aat	cag	aat	atc	ccc	ttc	ctc	act	ccc	ccc	ttt	96
Tyr	Gly	Tyr	Ala	Arg	Asn	Gln	Asn	Ile	Pro	Phe	Leu	Thr	Pro	Pro	Phe	
			20					25				30				
gtc	tcc	tcc	gat	gga	ttc	aaa	aac	ttc	ccc	cct	ggg	gta	ctg	tca	ctc	144
Val	Ser	Ser	Asp	Gly	Phe	Lys	Asn	Phe	Pro	Pro	Gly	Val	Leu	Ser	Leu	
			35				40					45				
aaa	ctg	gct	gat	cca	atc	acc	att	acc	aat	ggg	gat	gta	tcc	ctc	aag	192
Lys	Leu	Ala	Asp	Pro	Ile	Thr	Ile	Thr	Asn	Gly	Asp	Val	Ser	Leu	Lys	
			50			55				60						
gtg	gga	ggt	ggt	ctc	act	ttg	caa	gat	gga	agc	cta	act	gta	aac	cct	240
Val	Gly	Gly	Gly	Leu	Thr	Leu	Gln	Asp	Gly	Ser	Leu	Thr	Val	Asn	Pro	
				70					75					80		
aag	gct	cca	ctg	caa	gtt	act	act	gat	aaa	aaa	ctt	gag	ctt	gca	tat	288
Lys	Ala	Pro	Leu	Gln	Val	Thr	Thr	Asp	Lys	Lys	Leu	Glu	Leu	Ala	Tyr	
				85				90						95		
gat	aat	cca	ttt	gaa	tgt	agt	gct	aat	aaa	ttt	agt	tta	aaa	gta	gga	336
Asp	Asn	Pro	Phe	Glu	Cys	Ser	Ala	Asn	Lys	Phe	Ser	Leu	Lys	Val	Gly	
			100					105					110			

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cat His	gga Gly	tta Leu	aaa Lys	gta Val	tta Leu	gat Asp	gaa Glu	aaa Lys	agt Ser	gct Ala	gcg Ala	ggg Gly	tta Leu	aaa Lys	gat Asp	384
		115					120					125				
tta Leu	att Ile	ggc Gly	aaa Lys	ctt Leu	gtg Val	gtt Val	tta Leu	aca Thr	gga Gly	aaa Lys	gga Gly	ata Ile	ggc Gly	act Thr	gaa Glu	432
	130					135					140					
aat Asn	tta Leu	gaa Glu	aat Asn	aca Thr	gat Asp	ggt Gly	agc Ser	agc Ser	aga Arg	gga Gly	att Ile	ggt Gly	ata Ile	aat Asn	gta Val	480
145					150					155					160	
aga Arg	gca Ala	aga Arg	gaa Glu	ggg Gly	ttg Leu	aca Thr	ttt Phe	gac Asp	aat Asn	gat Asp	gga Gly	tac Tyr	ttg Leu	gta Val	gca Ala	528
				165				170					175			
tgg Trp	aac Asn	cca Pro	aag Lys	tat Tyr	gac Asp	acg Thr	cgc Arg	aca Thr	ctt Leu	tgg Trp	aca Thr	aca Thr	cca Pro	gac Asp	aca Thr	576
			180				185						190			
tct Ser	cca Pro	aac Asn	tgc Cys	aca Thr	att Ile	gct Ala	cag Gln	gat Asp	aag Lys	gac Asp	tct Ser	aaa Lys	ctc Leu	act Thr	ttg Leu	624
		195					200					205				
gta Val	ctt Leu	aca Thr	aag Lys	tgt Cys	gga Gly	agt Ser	caa Gln	ata Ile	tta Leu	gct Ala	aat Asn	gtg Val	tct Ser	ttg Leu	att Ile	672
	210					215					220					
gtg Val	gtc Val	gca Ala	gga Gly	aag Lys	tac Tyr	cac His	atc Ile	ata Ile	aat Asn	aat Asn	aag Lys	aca Thr	aat Asn	cca Pro	gaa Glu	720
225					230					235					240	
ata Ile	aaa Lys	agt Ser	ttt Phe	act Thr	att Ile	aaa Lys	ctg Leu	tta Leu	ttt Phe	aat Asn	aag Lys	aac Asn	gga Gly	gtg Val	ctt Leu	768
				245					250					255		
tta Leu	gac Asp	aac Asn	tca Ser	aat Asn	ctt Leu	gga Gly	aaa Lys	gct Ala	tat Tyr	tgg Trp	aac Asn	ttt Phe	aga Arg	agt Ser	gga Gly	816
			260					265					270			
aat Asn	tcc Ser	aat Asn	gtt Val	tcg Ser	aca Thr	gct Ala	tat Tyr	gaa Glu	aaa Lys	gca Ala	att Ile	ggt Gly	ttt Phe	atg Met	cct Pro	864
		275					280					285				
aat Asn	tta Leu	gta Val	gcg Ala	tat Tyr	cca Pro	aaa Lys	ccc Pro	agt Ser	aat Asn	tct Ser	aaa Lys	aaa Lys	tat Tyr	gca Ala	aga Arg	912
	290					295					300					
gac Asp	ata Ile	gtt Val	tat Tyr	gga Gly	act Thr	ata Ile	tat Tyr	ctt Leu	ggt Gly	gga Gly	aaa Lys	cct Pro	gat Asp	cag Gln	cca Pro	960
305					310				315						320	
gca Ala	gtc Val	att Ile	aaa Lys	act Thr	acc Thr	ttt Phe	aac Asn	caa Gln	gaa Glu	act Thr	gga Gly	tgt Cys	gaa Glu	tac Tyr	tct Ser	1008
				325					330					335		
atc Ile	aca Thr	ttt Phe	gac Asp	ttt Phe	agt Ser	tgg Trp	tcc Ser	aaa Lys	acc Thr	tat Tyr	gaa Glu	aat Asn	gtt Val	gaa Glu	ttt Phe	1056
			340					345					350			
gaa acc	acc acc	tct tct	ttt acc	ttc acc	tcc acc	tat att	gcc gaa	caa gaa	tga tga							1098

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Glu Thr Thr Ser Phe Thr Phe Ser Tyr Ile Ala Gln Glu *

355 360 365

<210> 39
 <211> 365
 <212> PRT
 <213> Adenovirus serotype 19p fiber

<400> 39
 Met Ser Lys Arg Leu Arg Val Glu Asp Asp Phe Asn Pro Val Tyr Pro
 1 5 10 15
 Tyr Gly Tyr Ala Arg Asn Gln Asn Ile Pro Phe Leu Thr Pro Pro Phe
 20 25 30
 Val Ser Ser Asp Gly Phe Lys Asn Phe Pro Pro Gly Val Leu Ser Leu
 35 40 45
 Lys Leu Ala Asp Pro Ile Thr Ile Thr Asn Gly Asp Val Ser Leu Lys
 50 55 60
 Val Gly Gly Gly Leu Thr Leu Gln Asp Gly Ser Leu Thr Val Asn Pro
 65 70 75 80
 Lys Ala Pro Leu Gln Val Thr Thr Asp Lys Lys Leu Glu Leu Ala Tyr
 85 90 95
 Asp Asn Pro Phe Glu Cys Ser Ala Asn Lys Phe Ser Leu Lys Val Gly
 100 105 110
 His Gly Leu Lys Val Leu Asp Glu Lys Ser Ala Ala Gly Leu Lys Asp
 115 120 125
 Leu Ile Gly Lys Leu Val Val Leu Thr Gly Lys Gly Ile Gly Thr Glu
 130 135 140
 Asn Leu Glu Asn Thr Asp Gly Ser Ser Arg Gly Ile Gly Ile Asn Val
 145 150 155 160
 Arg Ala Arg Glu Gly Leu Thr Phe Asp Asn Asp Gly Tyr Leu Val Ala
 165 170 175
 Trp Asn Pro Lys Tyr Asp Thr Arg Thr Leu Trp Thr Thr Pro Asp Thr
 180 185 190
 Ser Pro Asn Cys Thr Ile Ala Gln Asp Lys Asp Ser Lys Leu Thr Leu
 195 200 205
 Val Leu Thr Lys Cys Gly Ser Gln Ile Leu Ala Asn Val Ser Leu Ile
 210 215 220
 Val Val Ala Gly Lys Tyr His Ile Ile Asn Asn Lys Thr Asn Pro Glu
 225 230 235 240
 Ile Lys Ser Phe Thr Ile Lys Leu Leu Phe Asn Lys Asn Gly Val Leu
 245 250 255
 Leu Asp Asn Ser Asn Leu Gly Lys Ala Tyr Trp Asn Phe Arg Ser Gly
 260 265 270
 Asn Ser Asn Val Ser Thr Ala Tyr Glu Lys Ala Ile Gly Phe Met Pro
 275 280 285
 Asn Leu Val Ala Tyr Pro Lys Pro Ser Asn Ser Lys Lys Tyr Ala Arg
 290 295 300
 Asp Ile Val Tyr Gly Thr Ile Tyr Leu Gly Gly Lys Pro Asp Gln Pro
 305 310 315 320
 Ala Val Ile Lys Thr Phe Asn Gln Glu Thr Gly Cys Glu Tyr Ser
 325 330 335
 Ile Thr Phe Asp Phe Ser Trp Ser Lys Thr Tyr Glu Asn Val Glu Phe
 340 345 350
 Glu Thr Thr Ser Phe Thr Phe Ser Tyr Ile Ala Gln Glu
 355 360 365

<210> 40
 <211> 1228

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<212> DNA

<213> Adenovirus serotype 9 fiber

<220>

<221> CDS

<222> (50) ... (1138)

<400> 40

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aaggggatgtc aaattcctgg tccacaattt tcattgtctt ccctctcag atg tca aag 58
                                     Met Ser Lys
                                     1

agg ctc cgg gtg gaa gat gac ttc aac ccc gtc tac ccc tat. ggc tac 106
Arg Leu 5 Arg Val Glu Asp Asp Phe Asn Pro Val Tyr Pro Tyr Gly Tyr
                                     10
                                     15

gcg cgg aat cag aat atc ccc ttc ctc act ccc ccc ttt gtc tcc tcc 154
Ala Arg Asn Gln Asn Ile Pro Phe Leu Thr Pro Pro Phe Val Ser Ser
20                                     25
                                     30
                                     35

gat gga ttc caa aac ttc ccc cct ggg gtc ctg tca ctc aaa cta gct 202
Asp Gly Phe Gln Asn Phe Pro Pro Gly Val Leu Ser Leu Lys Leu Ala
40                                     45
                                     50

gac cca ata gcc atc gtc aat ggg aat gtc tca ctc aaa gtg gga ggg 250
Asp Pro Ile Ala Ile Val Asn Gly Asn Val Ser Leu Lys Val Gly Gly
55                                     60
                                     65

ggt ctc act ttg caa gat gga act gga aaa cta aca gtc aat gct gat 298
Gly Leu Thr Leu Gln Asp Gly Thr Gly Lys Leu Thr Val Asn Ala Asp
70                                     75
                                     80

cca cct ttg caa ctt aca aac aac aaa tta ggg att gct ttg gac gct 346
Pro Pro Leu Gln Leu Thr Asn Asn Lys Leu Gly Ile Ala Leu Asp Ala
85                                     90
                                     95

cca ttt gat gtt ata gat aat aaa ctc aca ttg tta gcg ggc cat ggc 394
Pro Phe Asp Val Ile Asp Asn Lys Leu Thr Leu Leu Ala Gly His Gly
100                                     105
                                     110
                                     115

ttg tct att ata aca aaa gaa aca tca aca ctg cct ggc ttg agg aat 442
Leu Ser Ile Ile Thr Lys Glu Thr Ser Thr Leu Pro Gly Leu Arg Asn
120                                     125
                                     130

act ctt gta gta tta act gga aag ggt att gga aca gaa tca aca gat 490
Thr Leu Val Val Leu Thr Gly Lys Gly Ile Gly Thr Glu Ser Thr Asp
135                                     140
                                     145

aat ggc gga acg gta tgt gtt aga gtt gga gaa ggt ggc ggc tta tca 538
Asn Gly Gly Thr Val Cys Val Arg Val Gly Glu Gly Gly Gly Leu Ser
150                                     155
                                     160

ttt aat aat gat gga gac ttg gta gca ttt aat aaa aaa gaa gat aag 586
Phe Asn Asn Asp Gly Asp Leu Val Ala Phe Asn Lys Lys Glu Asp Lys
165                                     170
                                     175

cgc acc cta tgg aca act cca gac aca tct cca aat tgc aag att gat 634
Arg Thr Leu Trp Thr Thr Pro Asp Thr Ser Pro Asn Cys Lys Ile Asp
180                                     185
                                     190
                                     195

cag gat aag gac tct aag tta act ctg gtc ctt aca aag tgt gga agt 682

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Gln	Asp	Lys	Asp	Ser	Lys	Leu	Thr	Leu	Val	Leu	Thr	Lys	Cys	Gly	Ser		
				200					205					210			
caa	ata	ttg	gct	aat	gtg	tca	tta	att	gtc	gta	gat	ggg	aag	tac	aaa	730	
Gln	Ile	Leu	Ala	Asn	Val	Ser	Leu	Ile	Val	Val	Asp	Gly	Lys	Tyr	Lys		
			215					220					225				
att	atc	aat	aac	aat	act	caa	cca	gct	ctc	aaa	gga	ttt	acc	att	aaa	778	
Ile	Ile	Asn	Asn	Asn	Thr	Gln	Pro	Ala	Leu	Lys	Gly	Phe	Thr	Ile	Lys		
				230			235					240					
tta	ttg	ttt	gat	gaa	aat	gga	gta	ctt	atg	gaa	tct	tca	aat	ctt	ggg	826	
Leu	Leu	Phe	Asp	Glu	Asn	Gly	Val	Leu	Met	Glu	Ser	Ser	Asn	Leu	Gly		
	245					250					255						
aaa	tca	tat	tgg	aac	ttt	aga	aat	gaa	aat	tca	att	atg	tca	aca	gct	874	
Lys	Ser	Tyr	Trp	Asn	Phe	Arg	Asn	Glu	Asn	Ser	Ile	Met	Ser	Thr	Ala		
260					265					270					275		
tat	gaa	aaa	gct	att	gga	ttc	atg	cct	aat	ttg	gta	gcc	tat	cca	aaa	922	
Tyr	Glu	Lys	Ala	Ile	Gly	Phe	Met	Pro	Asn	Leu	Val	Ala	Tyr	Pro	Lys		
				280					285					290			
cct	acc	gct	ggc	tct	aaa	aaa	tat	gca	aga	gat	ata	gtt	tat	gga	aac	970	
Pro	Thr	Ala	Gly	Ser	Lys	Lys	Tyr	Ala	Arg	Asp	Ile	Val	Tyr	Gly	Asn		
			295					300					305				
atc	tac	ctt	ggg	gga	aag	cca	gat	caa	cca	gta	acc	att	aaa	act	acc	1018	
Ile	Tyr	Leu	Gly	Gly	Lys	Pro	Asp	Gln	Pro	Val	Thr	Ile	Lys	Thr	Thr		
		310					315					320					
ttt	aat	cag	gaa	act	gga	tgt	gaa	tat	tct	atc	aca	ttt	gat	ttt	agt	1066	
Phe	Asn	Gln	Glu	Thr	Gly	Cys	Glu	Tyr	Ser	Ile	Thr	Phe	Asp	Phe	Ser		
	325					330					335						
tgg	gcc	aag	act	tat	gta	aat	gtt	gaa	ttt	gaa	aca	acc	tct	ttt	acc	1114	
Trp	Ala	Lys	Thr	Tyr	Val	Asn	Val	Glu	Phe	Glu	Thr	Thr	Ser	Phe	Thr		
340					345					350				355			
ttt	tcc	tat	atc	gcc	caa	gaa	tga	aagaccaata	aacgtgtttt	tcattttcaaa	1168						
Phe	Ser	Tyr	Ile	Ala	Gln	Glu	*										
				360													

atctttcatgt atcttttattg attttttacac cagcacgggt agtcagtctc ccaccaccag 1228

<210> 41

<211> 362

<212> PRT

<213> Adenovirus serotype 9 fiber

<400> 41

Met	Ser	Lys	Arg	Leu	Arg	Val	Glu	Asp	Asp	Phe	Asn	Pro	Val	Tyr	Pro
1				5					10					15	
Tyr	Gly	Tyr	Ala	Arg	Asn	Gln	Asn	Ile	Pro	Phe	Leu	Thr	Pro	Pro	Phe
			20					25					30		
Val	Ser	Ser	Asp	Gly	Phe	Gln	Asn	Phe	Pro	Pro	Gly	Val	Leu	Ser	Leu
		35					40					45			
Lys	Leu	Ala	Asp	Pro	Ile	Ala	Ile	Val	Asn	Gly	Asn	Val	Ser	Leu	Lys
	50					55					60				
Val	Gly	Gly	Gly	Leu	Thr	Leu	Gln	Asp	Gly	Thr	Gly	Lys	Leu	Thr	Val

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65	Asn	Ala	Asp	Pro	Pro	70	Leu	Gln	Leu	Thr	Asn	75	Asn	Lys	Leu	Gly	Ile	80	Ala
	Leu	Asp	Ala	Pro	85	Phe	Asp	Val	Ile	Asp	90	Asn	Lys	Leu	Thr	Leu	Leu	95	Ala
	Gly	His	Gly	Leu	100	Ser	Ile	Ile	Thr	105	Lys	Glu	Thr	Ser	Thr	Leu	Pro	110	Gly
	Leu	Arg	Asn	Thr	115	Leu	Val	Val	Leu	120	Thr	Gly	Lys	Gly	Ile	Gly	Thr	125	Glu
	Ser	Thr	Asp	Asn	130	Gly	Gly	Thr	Val	135	Cys	Val	Arg	Val	Gly	Glu	Gly	140	Gly
	Gly	Leu	Ser	Phe	145	Asn	Asn	Asp	Gly	150	Asp	Leu	Val	Ala	Phe	Asn	Lys	155	Lys
	Glu	Asp	Lys	Arg	165	Thr	Leu	Trp	Thr	170	Thr	Pro	Asp	Thr	Ser	Pro	Asn	175	Cys
	Lys	Ile	Asp	Gln	180	Asp	Lys	Asp	Ser	185	Lys	Leu	Thr	Leu	Val	Leu	Thr	190	Lys
	Cys	Gly	Ser	Gln	195	Ile	Leu	Ala	Asn	200	Val	Ser	Leu	Ile	Val	Val	Asp	205	Gly
	Lys	Tyr	Lys	Ile	210	Ile	Asn	Asn	Thr	215	Gln	Pro	Ala	Leu	Lys	Gly	Phe	220	Phe
	Thr	Ile	Lys	Leu	225	Leu	Phe	Asp	Glu	230	Asn	Gly	Val	Leu	Met	Glu	Ser	235	Ser
	Asn	Leu	Gly	Lys	245	Ser	Tyr	Trp	Asn	250	Phe	Arg	Asn	Glu	Asn	Ser	Ile	255	Met
	Ser	Thr	Ala	Tyr	260	Glu	Lys	Ala	Ile	265	Gly	Phe	Met	Pro	Asn	Leu	Val	270	Ala
	Tyr	Pro	Lys	Pro	275	Thr	Ala	Gly	Ser	280	Lys	Lys	Tyr	Ala	Arg	Asp	Ile	285	Val
	Tyr	Gly	Asn	Ile	290	Tyr	Leu	Gly	Gly	295	Lys	Pro	Asp	Gln	Pro	Val	Thr	300	Ile
	Lys	Thr	Thr	Phe	305	Asn	Gln	Glu	Thr	310	Gly	Cys	Glu	Tyr	Ser	Ile	Thr	315	Phe
	Asp	Phe	Ser	Trp	325	Ala	Lys	Thr	Tyr	330	Val	Asn	Val	Glu	Phe	Glu	Thr	335	Thr
	Ser	Phe	Thr	Phe	340	Ser	Tyr	Ile	Ala	345	Gln	Glu						350	
					355					360									

<210> 42
 <211> 20
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Ad2 third repeat

<400> 42
 Gly Asn Leu Thr Ser Gln Asn Val Thr Thr Val Thr Gln Pro Leu Lys
 1 5 10 15
 Lys Thr Lys Ser
 20

<210> 43
 <211> 20
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Ad5 third repeat

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<400> 43
 Gly Asn Leu Thr Ser Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys
 1 5 10 15
 Lys Thr Lys Ser
 20

<210> 44
 <211> 4
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Repeat motif
 <221> VARIANT
 <222> 4
 <223> Xaa = Thr or Ser

<400> 44
 Thr Thr Val Xaa
 1

<210> 45
 <211> 15
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Repeat Consensus Sequence

<221> VARIANT
 <222> 3,5,7,13
 <223> Xaa = Hydrophobic Amino Acid

<221> VARIANT
 <222> 1, 2, 4, 6, 8, 9, 11, 12, 14, 15
 <223> Xaa = Any Amino Acid

<221> VARIANT
 <222> 10
 <223> Xaa = Pro or Gly

<400> 45
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 1 5 10 15

<210> 46
 <211> 16
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Ad2 21st repeat

<400> 46
 Gly Ala Met Ile Thr Lys Leu Gly Ala Gly Leu Ser Phe Asp Asn Ser
 1 5 10 15

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<210> 47
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Ad5 21st repeat

<400> 47
Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp Ser Thr
1 5 10 15

<210> 48
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Ad37 last repeat

<400> 48
Ile Gly Ile Asn Val Arg Ala Arg Glu Gly Leu Thr Phe Asp Asn Asp
1 5 10 15

<210> 49
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Last repeat consensus sequence

<221> VARIANT
<222> 4,7
<223> Xaa = Any Amino Acid

<221> VARIANT
<222> 9
<223> Xaa = Asp or Asn

<400> 49
Lys Leu Gly Xaa Gly Leu Xaa Phe Xaa
1 5

<210> 50
<211> 1164
<212> DNA
<213> Artificial Sequence

<220>
<223> Ad5Ds fiber

<221> CDS
<222> (13)...(1092)

<221> misc_feature
<222> 1130, 1157
<223> n = A,T,C or G

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<400> 50

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atgggatcca ag atg aag cgc gca aga ccg tct gaa gat acc ttc aac ccc 51
      Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro
        1              5              10

gtg tat cca tat gac acg gaa acc ggt cct cca act gtg cct ttt ctt 99
Val Tyr Pro Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu
      15              20              25

act cct ccc ttt gta tcc ccc aat ggg ttt caa gag agt ccc cct ggg 147
Thr Pro Pro Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly
      30              35              40              45

gta ctc tct ttg cgc cta tcc gaa cct cta gtt acc tcc aat ggc atg 195
Val Leu Ser Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met
      50              55              60

ctt gcg ctc aaa atg ggc aac ggc ctc tct ctg gac gag gcc ggc aac 243
Leu Ala Leu Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn
      65              70              75

ctt acc tcc caa aat gta acc act gtg agc cca cct ctc aaa aaa acc 291
Leu Thr Ser Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr
      80              85              90

aag aaa aag ctt gaa gtt aac cta agc act gcc aag ggg ttg atg ttt 339
Lys Lys Lys Leu Glu Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe
      95              100              105

gac gct aca gcc ata gcc att aat gca gga gat ggg ctt gaa ttt ggt 387
Asp Ala Thr Ala Ile Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly
      110              115              120              125

tca cct aat gca cca aac aca aat ccc ctc aaa aca aaa att ggc cat 435
Ser Pro Asn Ala Pro Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His
      130              135              140

ggc cta gaa ttt gat tca aac aag gct atg gtt cct aaa cta gga act 483
Gly Leu Glu Phe Asp Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr
      145              150              155

ggc ctt agt ttt gac agc aca ggt gcc att aca gta gga aac aaa aat 531
Gly Leu Ser Phe Asp Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn
      160              165              170

aat gat aag cta act ttg tgg acc aca cca gct cca tct cct aac tgt 579
Asn Asp Lys Leu Thr Leu Trp Thr Thr Pro Ala Pro Ser Pro Asn Cys
      175              180              185

aga cta aat gca gag aaa gat gct aaa ctc act ttg gtc tta aca aaa 627
Arg Leu Asn Ala Glu Lys Asp Ala Lys Leu Thr Thr Leu Val Leu Thr Lys
      190              195              200              205

tgt ggc agt caa ata ctt gct aca gtt tca gtt ttg gct gtt aaa ggc 675
Cys Gly Ser Gln Ile Leu Ala Thr Val Ser Val Leu Ala Val Lys Gly
      210              215              220

agt ttg gct cca ata tct gga aca gtt caa agt gct cat ctt att ata 723
Ser Leu Ala Pro Ile Ser Gly Thr Val Gln Ser Ala His Leu Ile Ile
      225              230              235

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aga ttt gac gaa aat gga gtg cta cta aac aat tcc ttc ctg gac cca 771
Arg Phe Asp Glu Asn Gly Val Leu Asn Asn Ser Phe Leu Asp Pro
      240      245      250

gaa tat tgg aac ttt aga aat gga gat ctt act gaa ggc aca gcc tat 819
Glu Tyr Trp Asn Phe Arg Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr
      255      260      265

aca aac gct gtt gga ttt atg cct aac cta tca gct tat cca aaa tct 867
Thr Asn Ala Val Gly Phe Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser
      270      275      280      285

cac ggt aaa act gcc aaa agt aac att gtc agt caa gtt tac tta aac 915
His Gly Lys Thr Ala Lys Ser Asn Ile Val Ser Gln Val Tyr Leu Asn
      290      295      300

gga gac aaa act aaa cct gta aca cta acc att aca cta aac ggt aca 963
Gly Asp Lys Thr Lys Pro Val Thr Leu Thr Ile Thr Leu Asn Gly Thr
      305      310      315

cag gaa aca gga gac aca act cca agt gca tac tct atg tca ttt tca 1011
Gln Glu Thr Gly Asp Thr Thr Pro Ser Ala Tyr Ser Met Ser Phe Ser
      320      325      330

tgg gac tgg tct ggc cac aac tac att aat gaa ata ttt gcc aca tcc 1059
Trp Asp Trp Ser Gly His Asn Tyr Ile Asn Glu Ile Phe Ala Thr Ser
      335      340      345

tct tac act ttt tca tac att gcc caa gaa taa agaagcggcc gcggttatgaa 1112
Ser Tyr Thr Phe Ser Tyr Ile Ala Gln Glu *
      350      355

gggcgaattc cagcacantg gcggccgtta ttagtggatc cgagntcatg ca 1164

<210> 51
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Ad5deltas

<400> 51
Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro
1      5      10      15
Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro
20      25      30
Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser
35      40      45
Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu
50      55      60
Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser
65      70      75      80
Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Lys Lys
85      90      95
Leu Glu Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr
100      105      110
Ala Ile Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn
115      120      125
Ala Pro Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu
130      135      140

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Phe Asp Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser
 145 150 155 160
 Phe Asp Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys
 165 170 175
 Leu Thr Leu Trp Thr Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn
 180 185 190
 Ala Glu Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser
 195 200 205
 Gln Ile Leu Ala Thr Val Ser Val Leu Ala Val Lys Gly Ser Leu Ala
 210 215 220
 Pro Ile Ser Gly Thr Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp
 225 230 235 240
 Glu Asn Gly Val Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp
 245 250 255
 Asn Phe Arg Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala
 260 265 270
 Val Gly Phe Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys
 275 280 285
 Thr Ala Lys Ser Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys
 290 295 300
 Thr Lys Pro Val Thr Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr
 305 310 315 320
 Gly Asp Thr Thr Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp
 325 330 335
 Ser Gly His Asn Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr
 340 345 350
 Phe Ser Tyr Ile Ala Gln Glu
 355

<210> 52
 <211> 1920
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Ad5s/Ad37k fiber

<221> CDS
 <222> (13)...(1755)

<221> misc_feature
 <222> 1867, 1875
 <223> n = A,T,C or G

<400> 52
 gcaagatcca ag atg aag cgc gca aga ccg tct gaa gat acc ttc aac ccc 51
 Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro
 1 5 10
 gtg tat cca tat gac acg gaa acc ggt cct cca act gtg cct ttt ctt 99
 Val Tyr Pro Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu
 15 20 25
 act cct ccc ttt gta tcc ccc aat ggg ttt caa gag agt ccc cct ggg 147
 Thr Pro Pro Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly
 30 35 40 45
 gta ctc tct ttg cgc cta tcc gaa cct cta gtt acc tcc aat ggc atg 195
 Val Leu Ser Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met
 50 55 60

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ctt gcg ctc aaa atg ggc aac ggc ctc tct ctg gac gag gcc ggc aac	243
Leu Ala Leu Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn	
65 70 75	
ctt acc tcc caa aat gta acc act gtg agc cca cct ctc aaa aaa acc	291
Leu Thr Ser Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr	
80 85 90	
aag tca aac ata aac ctg gaa ata tct gca ccc ctc aca gtt acc tca	339
Lys Ser Asn Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser	
95 100 105	
gaa gcc cta act gtg gct gcc gcc gca cct cta atg gtc gcg ggc aac	387
Glu Ala Leu Thr Val Ala Ala Ala Pro Leu Met Val Ala Gly Asn	
110 115 120 125	
aca ctc acc atg caa tca cag gcc ccg cta acc gtg cac gac tcc aaa	435
Thr Leu Thr Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys	
130 135 140	
ctt agc att gcc acc caa gga ccc ctc aca gtg tca gaa gga aag cta	483
Leu Ser Ile Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu	
145 150 155	
gcc ctg caa aca tca ggc ccc ctc acc acc acc gat agc agt acc ctt	531
Ala Leu Gln Thr Ser Gly Pro Leu Thr Thr Thr Asp Ser Ser Thr Leu	
160 165 170	
act atc act gcc tca ccc cct cta act act gcc act ggt agc ttg ggc	579
Thr Ile Thr Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly	
175 180 185	
att gac ttg aaa gag ccc att tat aca caa aat gga aaa cta gga cta	627
Ile Asp Leu Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu	
190 195 200 205	
aag tac ggg gct cct ttg cat gta aca gac gac cta aac act ttg acc	675
Lys Tyr Gly Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr	
210 215 220	
gta gca act ggt cca ggt gtg act att aat aat act tcc ttg caa act	723
Val Ala Thr Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr	
225 230 235	
aaa gtt act gga gcc ttg ggt ttt gat tca caa ggc aat atg caa ctt	771
Lys Val Thr Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu	
240 245 250	
aat gta gca gga gga cta agg att gat tct caa aac aga cgc ctt ata	819
Asn Val Ala Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile	
255 260 265	
ctt gat gtt agt tat ccg ttt gat gct caa aac caa cta aat cta aga	867
Leu Asp Val Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg	
270 275 280 285	
cta gga cag ggc cct ctt ttt ata aac tca gcc cac aac ttg gat att	915
Leu Gly Gln Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile	
290 295 300	

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aac tac aac aaa ggc ctt tac ttg ttt aca gct tca aac aat tcc aaa Asn Tyr Asn Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys 305 310 315	963
aag ctt gag gtt aac cta agc act gcc aag ggg ttg atg ttt gac gct Lys Leu Glu Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala 320 325 330	1011
aca gcc ata gcc att aat gca gga gat ggg ctt gaa ttt ggt tca cct Thr Ala Ile Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro 335 340 345	1059
aat gca cca aac aca aat ccc ctc aaa aca aaa att ggc cat ggc cta Asn Ala Pro Asn Thr Asn Pro Leu Lys Thr Lys Ile Gly His Gly Leu 350 355 360 365	1107
gaa ttt gat tca aac aag gct atg gtt cct aaa cta gga act ggc ctt Glu Phe Asp Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu 370 375 380	1155
agt ttt gac agc aca ggt gcc att aca gta gga aac aaa aat aat gat Ser Phe Asp Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp 385 390 395	1203
aag cta act ttg tgg acc aca cca gac act agt cca aac tgc aca att Lys Leu Thr Leu Trp Thr Thr Pro Asp Thr Ser Pro Asn Cys Thr Ile 400 405 410	1251
gct caa gat aag gac tct aaa ctc act ttg gta ctt aca aag tgt gga Ala Gln Asp Lys Asp Ser Lys Leu Thr Leu Val Leu Thr Lys Cys Gly 415 420 425	1299
agt caa ata tta gct aat gtg tct ttg att gtg gtc gca gga aag tac Ser Gln Ile Leu Ala Asn Val Ser Leu Ile Val Val Ala Gly Lys Tyr 430 435 440 445	1347
cac atc ata aat aat aag aca aat cca aaa ata aaa agt ttt act att His Ile Ile Asn Asn Lys Thr Asn Pro Lys Ile Lys Ser Phe Thr Ile 450 455 460	1395
aaa ctg cta ttt aat aag aac gga gtg ctt tta gac aac tca aat ctt Lys Leu Leu Phe Asn Lys Asn Gly Val Leu Leu Asp Asn Ser Asn Leu 465 470 475	1443
gga aaa gct tat tgg aac ttt aga agt gga aat tcc aat gtt tcg aca Gly Lys Ala Tyr Trp Asn Phe Arg Ser Gly Asn Ser Asn Val Ser Thr 480 485 490	1491
gct tat gaa aaa gca att ggt ttt atg cct aat ttg gta gcg tat cca Ala Tyr Glu Lys Ala Ile Gly Phe Met Pro Asn Leu Val Ala Tyr Pro 495 500 505	1539
aaa ccc agt aat tct aaa aaa tat gca aga gac ata gtt tat gga act Lys Pro Ser Asn Ser Lys Lys Tyr Ala Arg Asp Ile Val Tyr Gly Thr 510 515 520 525	1587
ata tat ctt ggt gga aaa cct gat cag cca gca gtc att aaa act acc Ile Tyr Leu Gly Gly Lys Pro Asp Gln Pro Ala Val Ile Lys Thr Thr 530 535 540	1635
ttt aac caa gaa act gga tgt gaa tac tct atc aca ttt aac ttt agt	1683

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Phe Asn Gln Glu Thr Gly Cys Glu Tyr Ser Ile Thr Phe Asn Phe Ser
 545 550 555
 tgg tcc aaa acc tat gaa aat gtt gaa ttt gaa acc acc tct ttt acc 1731
 Trp Ser Lys Thr Tyr Glu Asn Val Glu Phe Glu Thr Thr Ser Phe Thr
 560 565 570
 ttc tcc tat att gcc caa gaa tga aaaagcggcc gctcgagtct agagggccccg 1785
 Phe Ser Tyr Ile Ala Gln Glu *
 575 580
 tttaaaccgcg ctgactcagcc tcgactgtgc cttctagttg ccagccatct gttgtttgcc 1845
 cctcccccggt gccttccttg ancctggaan gtgccactcc cactgtcctt tcctaataaa 1905
 atgaggaaat gcatac 1920

<210> 53
 <211> 580
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Ad5s/Ad37k

<400> 53
 Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr Pro
 1 5 10 15
 Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro
 20 25 30
 Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser
 35 40 45
 Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu
 50 55 60
 Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser
 65 70 75 80
 Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Ser Asn
 85 90 95
 Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu
 100 105 110
 Thr Val Ala Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr
 115 120 125
 Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile
 130 135 140
 Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln
 145 150 155
 Thr Ser Gly Pro Leu Thr Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr
 165 170 175
 Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu
 180 185 190
 Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly
 195 200 205
 Ala Pro Leu His Val Thr Asp Leu Asn Thr Leu Thr Val Ala Thr
 210 215 220
 Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr
 225 230 235
 Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala
 245 250 255
 Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val
 260 265 270
 Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln
 275 280 285
 Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn

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290
 Lys Gly Leu Tyr Leu Phe 295 Thr Ala Ser Asn Asn 300 Ser Lys Lys Leu Glu
 305 Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe 315 Asp Ala Thr Ala Ile
 325 Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro
 340 Leu Lys Thr Lys Ile Gly His Gly Leu 350 Phe Asp
 355 Asn Thr Asn Pro Leu Lys Thr Lys Leu Gly Thr Gly Leu Ser Phe Asp
 370 Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp
 385 Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn 380 Asn Asp Lys Leu Thr
 390 Leu Trp Thr Thr Pro Asp Thr Ser Pro Asn Cys Thr Ile Ala Gln Asp
 405 Lys Asp Ser Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile
 420 Leu Ala Asn Val Ser Leu Ile Val Val Ala Gly Lys Tyr His Ile Ile
 435 Asn Asn Lys Thr Asn Pro Lys Ile Lys Ser Phe Thr Ile Lys Leu Leu
 450 Phe Asn Lys Asn Gly Val Leu Leu Asp Asn Ser Asn Leu Gly Lys Ala
 465 Tyr Trp Asn Phe Arg Ser Gly Asn Ser Asn Val Ser Thr Ala Tyr Glu
 485 Lys Ala Ile Gly Phe Met Pro Asn Leu Val Ala Tyr Pro Lys Pro Ser
 500 Asn Ser Lys Lys Tyr Ala Arg Asp Ile Val Tyr Gly Thr Ile Tyr Leu
 515 Gly Gly Lys Pro Asp Gln Pro Ala Val Ile Lys Thr Thr Phe Asn Gln
 530 Glu Thr Gly Cys Glu Tyr Ser Ile Thr Phe Asn Phe Ser Trp Ser Lys
 545 Thr Tyr Glu Asn Val Glu Phe Glu Thr Thr Ser Phe Thr Phe Ser Tyr
 565 Ile Ala Gln Glu 570 575
 580

<210> 54
 <211> 1767
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Ad5s/Ad37s fiber

<221> CDS
 <222> (13)...(1749)

<400> 54
 atgggatcca ag atg aag cgc gca aga ccg tct gaa gat acc ttc aac ccc 51
 Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro
 1 5 10

gtg tat cca tat gac acg gaa acc ggt cct cca act gtg cct ttt ctt 99
 Val Tyr Pro Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu
 15 20 25

act cct ccc ttt gta tcc ccc aat ggg ttt caa gag agt ccc cct ggg 147
 Thr Pro Pro Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly

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30					35					40					45	
gta	ctc	tct	ttg	cgc	cta	tcc	gaa	cct	cta	gtt	acc	tcc	aat	ggc	atg	195
Val	Leu	Ser	Leu	Arg	Leu	Ser	Glu	Pro	Leu	Val	Thr	Ser	Asn	Gly	Met	
				50					55					60		
ctt	gcg	ctc	aaa	atg	ggc	aac	ggc	ctc	tct	ctg	gac	gag	gcc	ggc	agc	243
Leu	Ala	Leu	Lys	Met	Gly	Asn	Gly	Leu	Ser	Leu	Asp	Glu	Ala	Gly	Ser	
			65					70					75			
cta	act	gta	aac	cct	aag	gct	cca	ctg	caa	gtt	aat	act	gat	tca	aac	291
Leu	Thr	Val	Asn	Pro	Lys	Ala	Pro	Leu	Gln	Val	Asn	Thr	Asp	Ser	Asn	
		80					85					90				
ata	aac	ctg	gaa	ata	tct	gca	ccc	ctc	aca	gtt	acc	tca	gaa	gcc	cta	339
Ile	Asn	Leu	Glu	Ile	Ser	Ala	Pro	Leu	Thr	Val	Thr	Ser	Glu	Ala	Leu	
	95					100					105					
act	gtg	gct	gcc	gcc	gca	cct	cta	atg	gtc	gcg	ggc	aac	aca	ctc	acc	387
Thr	Val	Ala	Ala	Ala	Ala	Pro	Leu	Met	Val	Ala	Gly	Asn	Thr	Leu	Thr	
110					115				120					125		
atg	caa	tca	cag	gcc	ccg	cta	acc	gtg	cac	gac	tcc	aaa	ctt	agc	att	435
Met	Gln	Ser	Gln	Ala	Pro	Leu	Thr	Val	His	Asp	Ser	Lys	Leu	Ser	Ile	
				130					135					140		
gcc	acc	caa	gga	ccc	ctc	aca	gtg	tca	gaa	gga	aag	cta	gcc	ctg	caa	483
Ala	Thr	Gln	Gly	Pro	Leu	Thr	Val	Ser	Glu	Gly	Lys	Leu	Ala	Leu	Gln	
			145					150					155			
aca	tca	ggc	ccc	ctc	acc	acc	acc	gat	agc	agt	acc	ctt	act	atc	act	531
Thr	Ser	Gly	Pro	Leu	Thr	Thr	Thr	Asp	Ser	Ser	Thr	Leu	Thr	Ile	Thr	
		160					165					170				
gcc	tca	ccc	cct	cta	act	act	gcc	act	ggt	agc	ttg	ggc	att	gac	ttg	579
Ala	Ser	Pro	Pro	Leu	Thr	Thr	Ala	Thr	Gly	Ser	Leu	Gly	Ile	Asp	Leu	
	175					180					185					
aaa	gag	ccc	att	tat	aca	caa	aat	gga	aaa	cta	gga	cta	aag	tac	ggg	627
Lys	Glu	Pro	Ile	Tyr	Thr	Gln	Asn	Gly	Lys	Leu	Gly	Leu	Lys	Tyr	Gly	
190					195				200					205		
gct	cct	ttg	cat	gta	aca	gac	gac	cta	aac	act	ttg	acc	gta	gca	act	675
Ala	Pro	Leu	His	Val	Thr	Asp	Asp	Leu	Asn	Thr	Leu	Thr	Val	Ala	Thr	
				210					215				220			
ggt	cca	ggt	gtg	act	att	aat	aat	act	tcc	ttg	caa	act	aaa	gtt	act	723
Gly	Pro	Gly	Val	Thr	Ile	Asn	Asn	Thr	Ser	Leu	Gln	Thr	Lys	Val	Thr	
			225					230					235			
gga	gcc	ttg	ggt	ttt	gat	tca	caa	ggc	aat	atg	caa	ctt	aat	gta	gca	771
Gly	Ala	Leu	Gly	Phe	Asp	Ser	Gln	Gly	Asn	Met	Gln	Leu	Asn	Val	Ala	
		240					245					250				
gga	gga	cta	agg	att	gat	tct	caa	aac	aga	cgc	ctt	ata	ctt	gat	gtt	819
Gly	Gly	Leu	Arg	Ile	Asp	Ser	Gln	Asn	Arg	Arg	Leu	Ile	Leu	Asp	Val	
		255				260					265					
agt	tat	ccg	ttt	gat	gct	caa	aac	caa	cta	aat	cta	aga	cta	gga	cag	867
Ser	Tyr	Pro	Phe	Asp	Ala	Gln	Asn	Gln	Leu	Asn	Leu	Arg	Leu	Gly	Gln	
270					275					280					285	

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ggc Gly	cct Pro	ctt Leu	ttt Phe	ata Ile 290	aac Asn	tca Ser	gcc Ala	cac His	aac Asn 295	ttg Leu	gat Asp	att Ile	aac Asn	tac Tyr 300	aac Asn	915
aaa Lys	ggc Gly	ctt Leu	tac Tyr 305	ttg Leu	ttt Phe	aca Thr	gct Ala	tca Ser 310	aac Asn	aat Asn	tcc Ser	aaa Lys	aag Lys 315	ctt Leu	gag Glu	963
ggt Val	aac Asn	cta Leu 320	agc Ser	act Thr	gcc Ala	aag Lys	ggg Gly 325	ttg Leu	atg Met	ttt Phe	gac Asp	gct Ala 330	aca Thr	gcc Ala	ata Ile	1011
gcc Ala	att Ile 335	aat Asn	gca Ala	gga Gly	gat Asp	ggg Gly 340	ctt Leu	gaa Glu	ttt Phe	ggt Gly	tca Ser 345	cct Pro	aat Asn	gca Ala	cca Pro	1059
aac Asn 350	aca Thr	aat Asn	ccc Pro	ctc Leu	aaa Lys 355	aca Thr	aaa Lys	att Ile	ggc Gly	cat His 360	ggc Gly	cta Leu	gaa Glu	ttt Phe	gat Asp 365	1107
tca Ser	aac Asn	att Ile	ggt Gly	ata Ile 370	aat Asn	gta Val	aga Arg	gca Ala	aga Arg 375	gaa Glu	ggg Gly	ttg Leu	aca Thr	ttt Phe 380	gac Asp	1155
aat Asn	gat Asp	ggt Gly	gcc Ala 385	att Ile	aca Thr	gta Val	gga Gly	aac Asn 390	aaa Lys	aat Asn	aat Asn	gat Asp	aag Lys 395	cta Leu	act Thr	1203
ttg Leu	tgg Trp	acc Thr 400	aca Thr	cca Pro	gct Ala	cca Pro	tct Ser 405	cct Pro	aac Asn	tgt Cys	aga Arg	cta Leu 410	aat Asn	gca Ala	gag Glu	1251
aaa Lys	gat Asp 415	gct Ala	aaa Lys	ctc Leu	act Thr	ttg Leu 420	gtc Val	tta Leu	aca Thr	aaa Lys	tgt Cys 425	ggc Gly	agt Ser	caa Gln	ata Ile	1299
ctt Leu 430	gct Ala	aca Thr	ggt Val	tca Ser	ggt Val 435	ttg Leu	gct Ala	ggt Val	aaa Lys	ggc Gly 440	agt Ser	ttg Leu	gct Ala	cca Pro	ata Ile 445	1347
tct Ser	gga Gly	aca Thr	ggt Val	caa Gln 450	agt Ser	gct Ala	cat His	ctt Leu	att Ile 455	ata Ile	aga Arg	ttt Phe	gac Asp	gaa Glu 460	aat Asn	1395
gga Gly	gtg Val	cta Leu 465	cta Leu	aac Asn	aat Asn	tcc Ser	ttc Phe	ctg Leu 470	gac Asp	cca Pro	gaa Glu	tat Tyr	tgg Trp 475	aac Asn	ttt Phe	1443
aga Arg	aat Asn	gga Gly 480	gat Asp	ctt Leu	act Thr	gaa Glu	ggc Gly 485	aca Thr	gcc Ala	tat Tyr	aca Thr	aac Asn 490	gct Ala	ggt Val	gga Gly	1491
ttt Phe	atg Met 495	cct Pro	aac Asn	cta Leu	tca Ser	gct Ala 500	tat Tyr	cca Pro	aaa Lys	tct Ser	cac His 505	ggt Gly	aaa Lys	act Thr	gcc Ala	1539
aaa Lys 510	agt Ser	aac Asn	att Ile	gtc Val	agt Ser 515	caa Gln	ggt Val	tac Tyr	tta Leu	aac Asn 520	gga Gly	gac Asp	aaa Lys	act Thr	aaa Lys 525	1587

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[illegible]

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<210> 55
<211> 578
<212> PRT
<213> Artificial Sequence
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<220>
<223> Ad5s/Ad37s

<400>	55															
Met	Lys	Arg	Ala	Arg	Pro	Ser	Glu	Asp	Thr	Phe	Asn	Pro	Val	Tyr	Pro	
1				5					10					15		
Tyr	Asp	Thr	Glu	Thr	Gly	Pro	Pro	Thr	Val	Pro	Phe	Leu	Thr	Pro	Pro	
			20					25					30			
Phe	Val	Ser	Pro	Asn	Gly	Phe	Gln	Glu	Ser	Pro	Pro	Gly	Val	Leu	Ser	
		35					40					45				
Leu	Arg	Leu	Ser	Glu	Pro	Leu	Val	Thr	Ser	Asn	Gly	Met	Leu	Ala	Leu	
	50					55					60					
Lys	Met	Gly	Asn	Gly	Leu	Ser	Leu	Asp	Glu	Ala	Gly	Ser	Leu	Thr	Val	
65					70					75					80	
Asn	Pro	Lys	Ala	Pro	Leu	Gln	Val	Asn	Thr	Asp	Ser	Asn	Ile	Asn	Leu	
				85					90					95		
Glu	Ile	Ser	Ala	Pro	Leu	Thr	Val	Thr	Ser	Glu	Ala	Leu	Thr	Val	Ala	
			100					105					110			
Ala	Ala	Ala	Pro	Leu	Met	Val	Ala	Gly	Asn	Thr	Leu	Thr	Met	Gln	Ser	
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Gln	Ala	Pro	Leu	Thr	Val	His	Asp	Ser	Lys	Leu	Ser	Ile	Ala	Thr	Gln	
	130					135					140					
Gly	Pro	Leu	Thr	Val	Ser	Glu	Gly	Lys	Leu	Ala	Leu	Gln	Thr	Ser	Gly	
145					150					155					160	
Pro	Leu	Thr	Thr	Thr	Asp	Ser	Ser	Thr	Leu	Thr	Ile	Thr	Ala	Ser	Pro	
				165					170					175		
Pro	Leu	Thr	Thr	Ala	Thr	Gly	Ser	Leu	Gly	Ile	Asp	Leu	Lys	Glu	Pro	
			180					185					190			
Ile	Tyr	Thr	Gln	Asn	Gly	Lys	Leu	Gly	Leu	Lys	Tyr	Gly	Ala	Pro	Leu	
		195					200					205				
His	Val	Thr	Asp	Asp	Leu	Asn	Thr	Leu	Thr	Val	Ala	Thr	Gly	Pro	Gly	
	210					215					220					
Val	Thr	Ile	Asn	Asn	Thr	Ser	Leu	Gln	Thr	Lys	Val	Thr	Gly	Ala	Leu	
225					230					235					240	
Gly	Phe	Asp	Ser	Gln	Gly	Asn	Met	Gln	Leu	Asn	Val	Ala	Gly	Gly	Leu	
				245					250					255		
Arg	Ile	Asp	Ser	Gln	Asn	Arg	Arg	Leu	Ile	Leu	Asp	Val	Ser	Tyr	Pro	
			260					265					270			
Phe	Asp	Ala	Gln	Asn	Gln	Leu	Asn	Leu	Arg	Leu	Gly	Gln	Gly	Pro	Leu	

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275
 Phe Ile Asn Ser Ala His Asn 280
 290 Leu Asp Ile Asn Tyr 285
 Tyr Leu Phe Thr Ala Ser Asn 295
 305 Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile Ala Ile Asn
 310 315 320
 325 330 335
 Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro Asn Thr Asn
 340 345 350
 Pro Leu Lys Thr Lys Ile Gly His Gly Leu Glu Phe Asp Ser Asn Ile
 355 360 365
 Gly Ile Asn Val Arg Ala Arg Glu Gly Leu Thr Phe Asp Asn Asp Gly
 370 375 380
 Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr Leu Trp Thr
 385 390 395 400
 Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn Ala Glu Lys Asp Ala
 405 410 415
 Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile Leu Ala Thr
 420 425 430
 Val Ser Val Leu Ala Val Lys Gly Ser Leu Ala Pro Ile Ser Gly Thr
 435 440 445
 Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn Gly Val Leu
 450 455 460
 Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe Arg Asn Gly
 465 470 475 480
 Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly Phe Met Pro
 485 490 495
 Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala Lys Ser Asn
 500 505 510
 Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys Pro Val Thr
 515 520 525
 Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp Thr Thr Pro
 530 535 540
 Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly His Asn Tyr
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 Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser Tyr Ile Ala
 565 570 575
 Gln Glu

<210> 56
 <211> 1132
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Ad37s/Ad5k fiber

<221> CDS
 <222> (16)... (1116)

<221> misc_feature
 <222> 1125
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 Met Lys Arg Ala Arg Pro Ser Glu Asp Asp Phe Asn
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act ccc ccc ttt gtc tcc tcc gat gga ttc aaa aac ttc ccc cct ggg Thr Pro Pro Phe Val Ser Ser Asp Gly Phe Lys Asn Phe Pro Pro Gly 30 35 40	147
gta ctg tca ctc aaa ctg gct gat cca atc acc att acc aat ggg gat Val Leu Ser Leu Lys Leu Ala Asp Pro Ile Thr Ile Thr Asn Gly Asp 45 50 55 60	195
gta tcc ctc aag gtg gga ggt ggt ctc act ttg caa gat gga agc cta Val Ser Leu Lys Val Gly Gly Gly Leu Thr Leu Gln Asp Gly Ser Leu 65 70 75	243
act gta aac cct aag gct cca ctg caa gtt aat act gat aaa aaa ctt Thr Val Asn Pro Lys Ala Pro Leu Gln Val Asn Thr Asp Lys Lys Leu 80 85 90	291
gag ctt gca tat gat aat cca ttt gaa agt agt gct aat aaa ctt agt Glu Leu Ala Tyr Asp Asn Pro Phe Glu Ser Ser Ala Asn Lys Leu Ser 95 100 105	339
tta aaa gta gga cat gga tta aaa gta tta gat gaa aaa agt gct gcg Leu Lys Val Gly His Gly Leu Lys Val Leu Asp Glu Lys Ser Ala Ala 110 115 120	387
ggg tta aaa gat tta att ggc aaa ctt gtg gtt tta aca gga aaa gga Gly Leu Lys Asp Leu Ile Gly Lys Leu Val Val Leu Thr Gly Lys Gly 125 130 135 140	435
ata ggc act gaa aat tta gaa aat aca gat ggt agc agc aga gga att Ile Gly Thr Glu Asn Leu Glu Asn Thr Asp Gly Ser Ser Arg Gly Ile 145 150 155	483
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tac ttg gta gca tgg aac cca aag tat gac acg cgc act ttg tgg acc Tyr Leu Val Ala Trp Asn Pro Lys Tyr Asp Thr Arg Thr Leu Trp Thr 175 180 185	579
aca cca gct cca tct cct aac tgt aga cta aat gca gag aaa gat gct Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn Ala Glu Lys Asp Ala 190 195 200	627
aaa ctc act ttg gtc tta aca aaa tgt ggc agt caa ata ctt gct aca Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Ile Leu Ala Thr 205 210 215 220	675
ggt tca gtt ttg gct gtt aaa ggc agt ttg gct cca ata tct gga aca Val Ser Val Leu Ala Val Lys Gly Ser Leu Ala Pro Ile Ser Gly Thr 225 230 235	723
ggt caa agt gct cat ctt att ata aga ttt gac gaa aat gga gtg cta Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn Gly Val Leu 240 245 250	771
cta aac aat tcc ttc ctg gat cca gaa tat tgg aac ttt aga aat gga	819

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Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe Arg Asn Gly
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gat ctt act gaa ggc aca gcc tat aca aac gct gtt gga ttt atg cct      867
Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly Phe Met Pro
      270                                275                                280

aac cta tca gct tat cca aaa tct cac ggt aaa act gcc aaa agt aac      915
Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala Lys Ser Asn
      285                                290                                295                                300

att gtc agt caa gtt tac tta aac gga gac aaa act aaa cct gta aca      963
Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr Lys Pro Val Thr
      305                                310                                315

cta acc att aca cta aac ggt aca cag gaa aca gga gac aca act cca      1011
Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp Thr Thr Pro
      320                                325                                330

agt gca tac tct atg tca ttt tca tgg gac tgg tct ggc cac aac tac      1059
Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser Gly His Asn Tyr
      335                                340                                345

att aat gaa ata ttt gcc aca tcc tct tac act ttt tca tac att gcc      1107
Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Phe Ser Tyr Ile Ala
      350                                355                                360

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Gln Glu *
365

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 <211> 366
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Ad37s/Ad5k

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<400> 57
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Tyr Gly Tyr Ala Arg Asn Gln Asn Ile Pro Phe Leu Thr Pro Pro Phe
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Val Ser Ser Asp Gly Phe Lys Asn Phe Pro Pro Gly Val Leu Ser Leu
      35      40      45
Lys Leu Ala Asp Pro Ile Thr Ile Thr Asn Gly Asp Val Ser Leu Lys
      50      55      60
Val Gly Gly Gly Leu Thr Leu Gln Asp Gly Ser Leu Thr Val Asn Pro
      65      70      75      80
Lys Ala Pro Leu Gln Val Asn Thr Asp Lys Lys Leu Glu Leu Ala Tyr
      85      90      95
Asp Asn Pro Phe Glu Ser Ser Ala Asn Lys Leu Ser Leu Lys Val Gly
      100      105      110
His Gly Leu Lys Val Leu Asp Glu Lys Ser Ala Ala Gly Leu Lys Asp
      115      120      125
Leu Ile Gly Lys Leu Val Val Leu Thr Gly Lys Gly Ile Gly Thr Glu
      130      135      140
Asn Leu Glu Asn Thr Asp Gly Ser Ser Arg Gly Ile Gly Ile Asn Val
145      150      155      160

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Arg Ala Arg Glu Gly Leu Thr Phe Asp Asn Asp Gly Tyr Leu Val Ala
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Trp Asn Pro Lys Tyr Asp Thr Arg Thr Leu Trp Thr Thr Pro Ala Pro
      180      185
Ser Pro Asn Cys Arg Leu Asn Ala Glu Lys Asp Ala Lys Leu Thr Leu
      195      200      205
Val Leu Thr Lys Cys Gly Ser Gln Ile Leu Ala Thr Val Ser Val Leu
      210      215      220
Ala Val Lys Gly Ser Leu Ala Pro Ile Ser Gly Thr Val Gln Ser Ala
      225      230      235
His Leu Ile Ile Arg Phe Asp Glu Asn Gly Val Leu Leu Asn Asn Ser
      245      250      255
Phe Leu Asp Pro Glu Tyr Trp Asn Phe Arg Asn Gly Asp Leu Thr Glu
      260      265      270
Gly Thr Ala Tyr Thr Asn Ala Val Gly Phe Met Pro Asn Leu Ser Ala
      275      280      285
Tyr Pro Lys Ser His Gly Lys Thr Ala Lys Ser Asn Ile Val Ser Gln
      290      295      300
Val Tyr Leu Asn Gly Asp Lys Thr Lys Pro Val Thr Leu Thr Ile Thr
      305      310      315      320
Leu Asn Gly Thr Gln Glu Thr Gly Asp Thr Thr Pro Ser Ala Tyr Ser
      325      330      335
Met Ser Phe Ser Trp Asp Trp Ser Gly His Asn Tyr Ile Asn Glu Ile
      340      345      350
Phe Ala Thr Ser Ser Tyr Thr Phe Ser Tyr Ile Ala Gln Glu
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<210> 58
 <211> 16
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Ad37 third repeat

<400> 58
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<210> 59
 <211> 14
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Ad8 last repeat

<400> 59
 Val Arg Val Gly Glu Gly Gly Gly Leu Ser Phe Asn Asp Asn
 1 5 10

<210> 60
 <211> 14
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Ad9 last repeat

-47-

<400> 60
Val Arg Val Gly Glu Gly Gly Gly Leu Ser Phe Asn Asn Asp .
1 5 10

<210> 61
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Ad15 last repeat

<400> 61
Val Arg Val Gly Glu Gly Gly Gly Leu Ser Phe Asn Glu Ala
1 5 10

<210> 62
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Penton region

<400> 62
His Ala Ile Arg Gly Asp Thr Phe
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<210> 63
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Penton amino acid replacement

<400> 63
Ser Arg Gly Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Gly Thr Ser
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<210> 64
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Fiber protein conserved sequence

<400> 64
Thr Trp Leu Thr
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<210> 65
<211> 4
<212> PRT
<213> Artificial Sequence

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<220>
 <223> HSP binding motif

<400> 65
 Lys Lys Thr Lys
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<210> 66
 <211> 16
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Ad8 third repeat

<400> 66
 Gly Lys Leu Thr Val Asn Thr Glu Pro Pro Leu His Leu Thr Asn Asn
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<210> 67
 <211> 16
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Ad9 third repeat

<400> 67
 Gly Lys Leu Thr Val Asn Ala Asp Pro Pro Leu Gln Leu Thr Asn Asn
 1 5 10 15

<210> 68
 <211> 16
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Ad15 third repeat

<400> 68
 Gly Asn Leu Thr Val Asn Thr Glu Pro Pro Leu Gln Leu Thr Asn Asn
 1 5 10 15

<210> 69
 <211> 3929
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Vector pCR2.1

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 tcactcatta ggcaccccag gctttacact ttatgcttcc ggctcgtatg ttgtgtggaa 180
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 gtaccgagct cggatccact agtaacggcc gccagtgtgc tgggaattcgg ctttaagccga 300

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<220>
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<400> 70

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